

# **The high-resolution structure of the RNase P protein from *Thermotoga maritima* reveals a remarkable similarity among bacterial RNase P proteins.**

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RNase P, the ubiquitous endonuclease that catalyzes maturation of the 5'-end of tRNA, in Bacteria is a ribonucleoprotein particle composed of a large, catalytically active RNA and a small protein. Two major structural classes of RNase P RNA have been identified by phylogenetic comparative analysis, the A (ancestral) and B (*Bacillus*) types<sup>1</sup>. We have solved the X-ray crystal structure of the RNase P protein from the hyperthermophilic bacterium *T.maritima* at 1.3Å resolution<sup>2</sup>. This protein binds the A-type RNase P RNA.

In the crystal, the protein forms asymmetric dimers. In the light of substantial differences in the A and B-type RNAs, this protein structure bears remarkable similarity to the recently determined structures of RNase P proteins from organisms with B-type RNAs<sup>3</sup>. Structural conservation of potential RNA-binding elements in RNase P protein indicates that it binds to RNase P RNA primarily via direct contacts with the phylogenetically conserved core that is shared by A and B-classes of RNase P RNA.

In order to assess a potential physiological role for the protein dimerization, attempts to detect the dimerization in solution by light-scattering technique are currently in progress.

## **REFERENCES**

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This work has been supported by NIH grant GM34527.

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